Rahil Taujale | Curriculum Vitae

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Education

PhD in Bioinformatics — Institute of Bioinformatics, University of Georgia, Athens, GA (Current cGPA - 4.0) 2015 — present

Master of Science in Bioinformatics — Department of Biological Sciences, Northern Illinois University, DeKalb, IL (cGPA - 4.0) 2013 — 2015

Bachelor of Technology in Biotechnology — Kathmandu University, Dhulikhel, Kavre, Nepal (cGPA - 3.65) 2007 — 2011

Publications

Taujale R, Venkat A, Huang LC, Yeung W, Rasheed K, Edison AS, Moremen KW, Kannan N. **Deep evolutionary analysis reveals the design principles of fold A glycosyltransferases. (**bioRxiv: https://doi.org/10.1101/2019.12.31.891697; Under review, eLife) 2020

Bento AI, **Taujale R**, Schot C, Bosch T, Mariman R, King AA, Rohani P. **Phylodynamics of pertussis in the vaccine era: transition to re-emergence.** (medRxiv: https://doi.org/10.1101/19012138; In preparation) 2020

Beattie NR, Keul ND, Hicks Sirmans TN, McDonald WE, Talmadge TM, **Taujale R**, Kannan N, Wood ZA. **Conservation of Atypical Allostery in C. elegans UDP-Glucose Dehydrogenase**. ACS Omega, 2019 Sep 2.4;4(15):16318-16329. 2019

Florimond C, Cordonnier C, **Taujale R**, Wel HVD, Kannan N, West CM, Blader IJ. **A Toxoplasma Prolyl Hydroxylase Mediates Oxygen Stress Responses by Regulating Translation Elongation**. mBio, 2019. 10(2) 2019

Kwon A, Scott S, **Taujale R**, Yeung W, Kochut KJ, Eyers PA, Kannan N. **Tracing the origin and evolution of pseudokinases across the tree of life.** Science Signaling, 2019. 12 (578) 2019

Soares V, **Taujale R**, Garrett R, da Silva AJR, Borges RM. **Extending compound identification for molecular network using the LipidXplorer database independent method: A proof of concept using glycoalkaloids from *Solanum pseudoquina A. St.-Hi*.** Phytochemical Analysis, 2018. 2018

Borges RM, **Taujale R**, de Souza JS, de Andrade Bezerra T, Silva ELE, Herzog R, Ponce FV, Wolfender JL, Edison AS. **Dereplication of plant phenolics using a mass-spectrometry database independent method.** Phytochemical Analysis, 2018. 29(6):601-612 2018

Rahman K, Mandalasi M, Zhao P, Sheikh MO, **Taujale R**, Kim HW, Wel HVD, Matta K, Kannan N, Glushka JN, Wells L, West CM. **Characterization of a cytoplasmic glucosyltransferase that extends the core trisaccharide of the Toxoplasma Skp1 E3 ubiquitin ligase subunit**, Journal of Biological Chemistry, 2017. 292(45):18644-18659 2017

Hu L, **Taujale R**, Liu F, Song J, Yin Q, Zhang Y, Guo J, Yin Y. **Draft genome sequence of Talaromyces verruculosus ("Penicillium verruculosum") strain TS63-9, a fungus with great potential for industrial production of polysaccharide-degrading enzymes**, Journal of Biotechnology, 2016. 219:p.5-6 2016

Taujale R, Yin Y. **Glycosyltransferase Family 43 Is Also Found in Early Eukaryotes and Has Three Subfamilies in Charophycean Green Algae**, PloS One, 2015. 10(5) 2015

Ekstrom A, **Taujale R**, McGinn N, Yin Y. **PlantCAZyme: a database for plant carbohydrate-active enzymes**, Database: The Journal of Biological Databases and Curation, 2014. 2014

Conferences/ Workshops

2019 Annual Meeting of the Society for Glycobiology, Phoenix, AZ November 2-5, 2019
- Oral and Poster talks

Trees in the Desert 2019: A workshop on ultra-large phylogenetic trees, Tucson, AZ April 12-14, 2019
- Part of a working group to discuss current approaches and issues in building large phylogenies

RevBayes: Bayesian Inference of Phylogeny, NIMBioS Accelerated Tutorial, University of Tennessee, Knoxville August 7-11, 2017
- Discussion group for implementation of Bayesian methods towards phylogenetic inference

21st International *C. elegans* conference, University of California, Los Angeles June 21-25, 2017
- Poster talk

2016 Annual Meeting of the Society for Glycobiology, New Orleans, LA November 19-22, 2016
- Poster talk

Awards

3 Minute Thesis Competition Winner, 2017 UGA Institute of Bioinformatics Symposium: Parsing the Microbiome, University of Georgia September 25, 2017

Glycoscience Training Program Fellowship, Complex Carbohydrate Research Center, University of Georgia 2016

Sidney A. Mittler Award for Outstanding graduate student, Department of Biological Sciences, Northern Illinois University 2015

Community Involvement

Organizing Committee Member, Institute of Bioinformatics Spring Retreat 2018 April 2018

Treasurer, Nepalese Student Association October 2016 — October 2018

Member, Biotechnology Society of Nepal June 2009 — present

Vice President, Kathmandu University Biotechnology Creatives August 2008 — August 2009

Experience

Graduate Research Assistant — Evolutionary Systems Biology Lab (Kannan) and Small Molecules in Biology (Edison) labs, University of Georgia August 2015 — present

Research Assistant — Bioinformatics and Evolutionary Genomics Lab (Yin lab), Northern Illinois University July 2014 — August 2015

Teaching Assistant — Northern Illinois University Fall 2013 — Summer 2014
General Biology (BIOS 105)

Projects

An evolutionary systems approach to investigate sequence-structure-function relationships in Glycosyltransferases, University of Georgia (Dissertation project) — 2016 — present

An integrative pipeline for the processing, analysis and visualization of 1D NMR data, University of Georgia — 2016 — present

Detailed Study of the evolution of Plant CAZymes in *Klebsormidium flaccidum*, a recently sequenced charophytic green algae, Northern Illinois University (Research Assistant) — 2014 — 2015

Prediction of 3D structure and study of functional motifs for Arabidopsis CslA protein, Northern Illinois University (Research Assistant) — 2013 — 2014

An Integrative Evolutionary Analysis of Xylan Biosynthesis-related Glycosyltransferase Family 43, Northern Illinois University (Master's thesis) — 2013 — 2014

Skills

Computer

Programming languages — Perl, Python, MATLAB, MySQL, PHP, R, Bash scripting

Sequence alignment tools — BLAST, HMMER, MEGA, MAFFT, Muscle, T-coffee

Phylogenetic analysis tools — IQTree, RaxMs, PhyML, FastTree, Mr. Bayes, RevBayes

Next Generation Sequencing assembly and analysis tools — Velvet-oases, Trinity, Tuxedo suite, STAR, DESeq

Protein structure visualization and handling tools — PyMol, Chimera, AutoDock tools

Protein structure prediction, modelling and comparison tools — I-TASSER, Modeller, Rosetta, TM-Align

Languages

English (Proficient) Nepali (Proficient)

Newari (Proficient) Hindi (Competent)

Major Courses

Graduate School at UGA:

Statistical Inference for Bioinformatics, Algorithms for Computational Biology, Applied Genome Analysis, Glycobiology, Glycochemistry

Graduate School at NIU:

Programming for Bioinformatics, Databases, Recombinant DNA Techniques Laboratory, Biostatistics

Undergraduate:

Bioinformatics, Proteomics & Genomics, Protein Engineering, Quantitative Analysis, Instrumental Analysis

References can be provided upon request.